

Metrology for Marine Gene Expression – Environmental Biosensors

The development of microarray and other molecular technologies over the past decade has given investigators, managers, and public health agencies new and powerful tools to examine and monitor the impacts of environmental stresses in a host of species. These technologies offer the potential to develop rapid and highly sensitive means to monitor the health of living resources and the risks to human health. However, a lack of standards has slowed the exploitation of these technologies. NIST, in partnership with the Hollings Marine Laboratory (HML), is focusing on gene expression metrology and standards to underpin microarray technology to study oysters

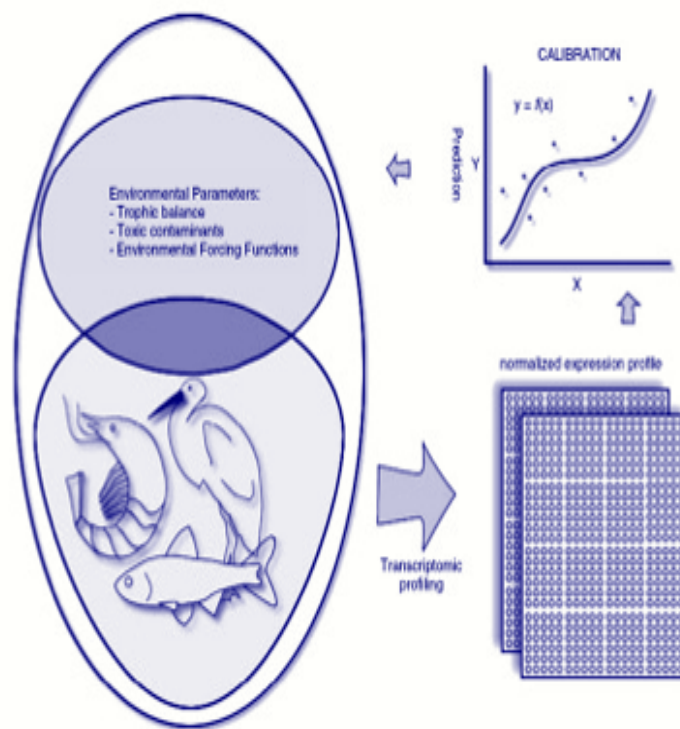
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In recent years a substantial decline in the population of the Eastern oyster, *Crassostrea virginica*, has occurred due to a variety of causes including over-harvesting, pollution, physical alterations of the habitat, and disease. An additional problem is the fact that the consumption of oysters from polluted waters poses a serious health risk. Specifically, oysters are known to harbor a variety of human pathogens and biomagnify a variety of contaminants. Public health agencies in all coastal states routinely monitor water quality for fecal coliforms, and organic and inorganic contaminants, but do not monitor oysters directly. The water quality assessments also do not include most human pathogens and a host of chemicals, for reasons that include difficulties and expense in assays procedures, lack of measurement standards, and acceptable risk thresholds.

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This year, genes were selected from *C. virginica* and *C. gigas* libraries based upon sequence homologies between the species, length of the homologous region, and distinction from other sequences in the selected suite. This was accomplished using expressed sequence tags (Chen, et. al., 2004). Further studies will involve amplifying and

purifying cDNAs for microarray printing, sequencing full length cDNA clones for molecular mass determinations, spotting arrays with varying concentrations (ng per spot and nM/L per spot), and hybridization of the arrays.



The diagram shows the universal environmental transcriptomic biosensor concept: expression microarrays probe the transcriptome of selected sentinel species for calibration, by machine learning, to the target environmental parameters.

Publications:

Almeida, J.S., McKillen, D.J., Chen, Y.A., Gross, P.S., Chapman, R.W., Warr, G. ***Design and calibration of microarrays as universal transcriptomic environmental biosensors. Comparative and Functional Genomics*** (2005) 6, 132-137.

Chen, Y.A., McKillen, D.J., Wu, S., Jenny, M.J., Chapman, R., Gross, P.S., Warr, G.W., Almeida, J.S. ***Optimal cDNA microarray design using expressed sequence tags for organisms with limited genomic information. BMC Bioinformatics*** (2004) 5, 191.